

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lee, Soo Y.  
Choi, Yongwon

(ii) TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER  
FAMILY, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.  
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Floor  
(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/052,089  
(B) FILING DATE: 31-MAR-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Pro Ile Arg Ala Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His

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15

Ser Arg Asp Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln  
20 25 30

Cys Leu Ile Gln Ser Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln  
35 40 45

Cys Arg Ile Gln Val Gly Lys Arg Thr Ile Ile Asn Lys Leu Phe Phe  
50 55 60

Asp Leu Ala Gln Glu Glu Glu Asn Val Leu Asp Arg Glu Phe Leu Lys  
65 70 75 80

Asn Glu Leu Asp Asn Val Arg Ala Gln Leu Ser Gln Lys Asp Lys Glu  
85 90 95

Lys Arg Asp Ser Gln Val Ile Ile Asp Thr Leu Arg Asp Thr Leu Glu  
100 105 110

Glu Arg Asn Ala Thr Val Val Ser Leu Gln Gln Ala Leu Gly Lys Ala  
115 120 125

Glu Met Leu Cys Ser Thr Leu Lys Lys Gln Met Lys Tyr Leu Glu Gln  
130 135 140

Gln Gln Asp Glu Thr Lys Gln Ala Gln Glu Glu Ala Gly Arg Leu Arg  
145 150 155 160

Ser Lys Met Lys Thr Met Glu Gln Ile Glu Leu Leu Leu Gln Ser Gln  
165 170 175

Leu Pro Glu Val Glu Glu Met Ile Arg Asp Met Gly Val Gly Gln Ser  
180 185 190

Ala Val Glu Gln Leu Ala Val Tyr Cys Val Ser Leu Lys Lys Glu Tyr  
195 200 205

Glu Asn Leu Lys Glu Ala Arg Lys Ala Ser Gly Glu Val Ala Asp Lys  
210 215 220

Leu Arg Lys Asp Leu Phe Ser Ser Arg Ser Lys Leu Gln Thr Val Tyr  
225 230 235 240

Ser Glu Leu Asp Gln Ala Lys Leu Glu Leu Lys Ser Ala Gln Lys Asp  
245 250 255

Leu Gln Ser Ala Asp Lys Glu Ile Met Ser Leu Lys Lys Lys Leu Thr  
260 265 270

Met Leu Gln Glu Thr Leu Asn Leu Pro Pro Val Ala Ser Glu Thr Val  
275 280 285

Asp Arg Leu Val Leu Glu Ser Pro Ala Pro Val Glu Val Asn Leu Lys  
290 295 300

Leu Arg Arg Pro Ser Phe Arg Asp Asp Ile Asp Leu Asn Ala Thr Phe  
305 310 315 320

Asp Val Asp Thr Pro Pro Ala Arg Pro Ser Ser Ser Gln His Gly Tyr  
325 330 335

Tyr Glu Lys Leu Cys Leu Glu Lys Ser His Ser Pro Ile Gln Asp Val  
340 345 350

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Pro Lys Lys Ile Cys Lys Gly Pro Arg Lys Glu Ser Gln Leu Ser Leu  
355 360 365

Gly Gly Gln Ser Cys Ala Gly Glu Pro Asp Glu Glu Leu Val Gly Ala  
370 375 380

Phe Pro Ile Phe Val Arg Asn Ala Ile Leu Gly Gln Lys Gln Pro Lys  
385 390 395 400

Arg Pro Arg Ser Glu Ser Ser Cys Ser Lys Asp Val Val Arg Thr Gly  
405 410 415

Phe Asp Gly Leu Gly Gly Arg Thr Lys Phe Ile Gln Pro Thr Asp Thr  
420 425 430

Val Met Ile Arg Pro Leu Pro Val Lys Pro Lys Thr Lys Val Lys Gln  
435 440 445

Arg Val Arg Val Lys Thr Val Pro Ser Leu Phe Gln Ala Lys Leu Asp  
450 455 460

Thr Phe Leu Trp Ser  
465

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Ile Leu Ser Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His  
1 5 10 15

Ser Arg Asp Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln  
20 25 30

Cys Leu Ile Gln Trp Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln  
35 40 45

Cys Arg Ile Gln Val Gly Lys Lys Thr Ile Ile Asn Lys Leu Phe Phe  
50 55 60

Asp Leu Ala Gln Glu Glu Glu Asn Val Leu Asp Ala Glu Phe Leu Lys  
65 70 75 80

Asn Glu Leu Asp Ser Val Lys Ala Gln Leu Ser Gln Lys Asp Arg Glu  
85 90 95

Lys Arg Asp Ser Gln Ala Ile Ile Asp Thr Leu Arg Asp Thr Leu Glu  
100 105 110

Glu Arg Asn Ala Thr Val Glu Ser Leu Gln Asn Ala Leu Asn Lys Ala  
 115 120 125  
 Glu Met Leu Cys Ser Thr Leu Lys Lys Gln Met Lys Phe Leu Glu Gln  
 130 135 140  
 Arg Gln Asp Glu Thr Lys Gln Ala Arg Glu Glu Ala His Arg Leu Lys  
 145 150 155 160  
 Cys Lys Met Lys Thr Met Glu Gln Ile Glu Leu Leu Leu Gln Ser Gln  
 165 170 175  
 Arg Ser Glu Val Glu Glu Met Ile Arg Asp Met Gly Val Gly Gln Ser  
 180 185 190  
 Ala Val Glu Gln Leu Ala Val Tyr Cys Val Ser Leu Lys Lys Glu Tyr  
 195 200 205  
 Glu Asn Leu Lys Glu Ala Arg Lys Ala Thr Gly Glu Leu Ala Asp Arg  
 210 215 220  
 Leu Lys Lys Asp Leu Val Ser Ser Arg Ser Lys Leu Lys Thr Leu Asn  
 225 230 235 240  
 Thr Glu Leu Asp Gln Ala Lys Leu Glu Leu Arg Ser Ala Gln Lys Asp  
 245 250 255  
 Leu Gln Ser Ala Asp Gln Glu Ile Thr Ser Leu Arg Lys Lys Ser Asp  
 260 265 270  
 Asp Pro Pro Gly Asn Leu Glu Pro Ala Ser Ala Thr Asn Glu Thr Val  
 275 280 285  
 Ser Arg Leu Val Phe Glu Ser Pro Ala Pro Val Glu Met Met Asn Pro  
 290 295 300  
 Arg Leu His Gln Pro Pro Phe Gly Asp Glu Ile Asp Leu Asn Thr Thr  
 305 310 315 320  
 Phe Asp Val Asn Thr Pro Pro Thr Gln Thr Ser Gly Ser Gln His Cys  
 325 330 335  
 Leu Pro Lys Lys Leu Cys Leu Glu Arg Ala Arg Ser Pro Met Gln Asn  
 340 345 350  
 Val Leu Lys Lys Val His Lys Val Ser Lys Pro Glu Ser Gln Leu Ser  
 355 360 365  
 Leu Gly Gly Gln Arg Cys Val Gly Glu Leu Asp Glu Glu Leu Ala Gly  
 370 375 380  
 Ala Phe Pro Leu Phe Ile Arg Asn Ala Val Leu Gly Gln Lys Gln Pro  
 385 390 395 400  
 Asn Arg Thr Thr Ala Glu Ser Arg Ser Ser Thr Asp Val Val Arg Ile  
 405 410 415  
 Gly Phe Asp Gly Leu Gly Gly Arg Thr Lys Phe Ile Gln Pro Arg Asp  
 420 425 430  
 Thr Thr Ile Ile Arg Pro Val Pro Val Lys Ser Lys Ala Lys Ser Lys  
 435 440 445  
 Gln Lys Val Arg Ile Lys Thr Val Ser Ser Ala Ser Gln Pro Lys Leu  
 450 455 460

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Asp Thr Phe Leu Cys Gln  
465 470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Thr Ile Ile Asn Lys Leu Phe Phe Asp Leu Ala Gln Glu Glu Glu  
1 5 10 15  
Asn Val Leu Asp Arg Glu Phe Leu Lys Asn Glu Leu Asp Asn Val Arg  
20 25 30  
Ala Gln Leu Ser Gln Lys Asp Lys Glu Lys Arg Asp Ser Gln Val Ile  
35 40 45  
Ile Asp Thr Leu Arg Asp Thr Leu Glu Glu Arg Asn Ala Thr Val Val  
50 55 60  
Ser Leu Gln Gln Ala Leu Gly Lys Ala Glu Met Leu Cys Ser Thr Leu  
65 70 75 80  
Lys Lys Gln Met Lys Tyr Leu Glu Gln Gln Gln Asp Glu Thr Lys Gln  
85 90 95  
Ala Gln Glu Glu Ala Gly Arg Leu Arg Ser Lys Met Lys Thr Met Glu  
100 105 110  
Gln Ile Glu Leu Leu Leu Gln Ser Gln Leu Pro Glu Val Glu Glu Met  
115 120 125  
Ile Arg Asp Met Gly Val Gly Gln Ser Ala Val Glu Gln Leu Ala Val  
130 135 140  
Tyr Cys Val Ser Leu Lys Lys Glu Tyr Glu Asn Leu Lys Glu Ala Arg  
145 150 155 160  
Lys Ala Ser Gly Glu Val Ala Asp Lys Leu Arg Lys Asp Leu Phe Ser  
165 170 175  
Ser Arg Ser Lys Leu Gln Thr Val Tyr Ser Glu Leu Asp Gln Ala Lys  
180 185 190  
Leu Glu Leu Lys Ser Ala Gln Lys Asp Leu Gln Ser Ala Asp Lys Glu  
195 200 205  
Ile Met Ser Leu Lys Lys Lys Leu Thr Met Leu Gln  
210 215 220

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Thr Ile Ile Asn Lys Leu Phe Phe Asp Leu Ala Gln Glu Glu Glu  
1 5 10 15  
Asn Val Leu Asp Ala Glu Phe Leu Lys Asn Glu Leu Asp Ser Val Lys  
20 25 30  
Ala Gln Leu Ser Gln Lys Asp Arg Glu Lys Arg Asp Ser Gln Ala Ile  
35 40 45  
Ile Asp Thr Leu Arg Asp Thr Leu Glu Glu Arg Asn Ala Thr Val Glu  
50 55 60  
Ser Leu Gln Asn Ala Leu Asn Lys Ala Glu Met Leu Cys Ser Thr Leu  
65 70 75 80  
Lys Lys Gln Met Lys Phe Leu Glu Gln Arg Gln Asp Glu Thr Lys Gln  
85 90 95  
Ala Arg Glu Glu Ala His Arg Leu Lys Cys Lys Met Lys Thr Met Glu  
100 105 110  
Gln Ile Glu Leu Leu Leu Gln Ser Gln Arg Ser Glu Val Glu Glu Met  
115 120 125  
Ile Arg Asp Met Gly Val Gly Gln Ser Ala Val Glu Gln Leu Ala Val  
130 135 140  
Tyr Cys Val Ser Leu Lys Lys Glu Tyr Glu Asn Leu Lys Glu Ala Arg  
145 150 155 160  
Lys Ala Thr Gly Glu Leu Ala Asp Arg Leu Lys Lys Asp Leu Val Ser  
165 170 175  
Ser Arg Ser Lys Leu Lys Thr Leu Asn Thr Glu Leu Asp Gln Ala Lys  
180 185 190  
Leu Glu Leu Arg Ser Ala Gln Lys Asp Leu Gln Ser Ala Asp Gln Glu  
195 200 205  
Ile Thr Ser Leu Arg Lys Lys Ser Asp Asp Pro Pro  
210 215 220

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Ala Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His Ser Arg Asp  
1 5 10 15  
Val Ala Ala Met Asp Cys Gly His Thr Phe His Leu Gln Cys Leu Ile  
20 25 30  
Gln Ser Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln Cys Arg Ile  
35 40 45  
Gln Val Gly  
50

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Ser Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His Ser Arg Asp  
1 5 10 15  
Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln Cys Leu Ile  
20 25 30  
Gln Trp Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln Cys Arg Ile  
35 40 45  
Gln Val Gly  
50

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2007 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCGGTGGA GCGAAATTTG AAGCAAGCGG AGGCGGGGCG CTCTACGAAG CCGGACCTGT 60  
AGCAGTTTCT TTGGCTGCCT GGGCCCCTTG AGTCCAGCCA TCATGCCTAT CCGTGCTCTG 120  
TGCATATCT GCTCCGACTT CTTGATCAC TCCCGGACG TGGCCGCCAT CCACTGCGGC 180  
CACACCTTCC ACTTGCAGTG CCTAATTCAG TCCTTTGAGA CAGCACCAAG TCGGACCTGC 240  
CCACAGTGCC GAATCCAGGT TGGCAAAGA ACCATTATCA ATAAGCTCTT CTTTGATCTT 300  
GCCCAGGAGG AGGAGAATGT CTTGGATCGA GAATTCTTAA AGAATGAAGT GGACAATGTC 360  
AGAGCCCAGC TTTCCCAGAA AGACAAGGAG AAACGAGACA GCCAGGTCAT CATCGACACT 420  
CTGCGGGATA CGCTGGAAGA ACGCAATGCT ACTGTGGTAT CTCTGCAGCA GGCCTTGGGC 480  
AAGGCCGAGA TGCTGTGCTC CACACTGAAA AAGCAGATGA AGTACTTAGA GCAGCAGCAG 540  
GATGAGACCA AACAAGCACA AGAGGAGGCG GGCCGGCTCA GGAGCAAGAT GAAGACCATG 600  
GAGCAGATTG AGCTTCTACT CCAGAGCCAG CTCCCTGAGG TGGAGGAGAT GATCCGAGAC 660  
ATGGGTGTGG GACAGTCAGC GGTGGAACAG CTGGCTGTGT ACTGTGTGTC TCTCAAGAAA 720  
GAGTACGAGA ATCTAAAAGA GGCACGGAAG GCCTCAGGGG AGGTGGCTGA CAAGCTGAGG 780  
AAGGATTTGT TTTCTCCAG AAGCAAGTTG CAGACAGTCT ACTCTGAATT GGATCAGGCC 840  
AAGTTAGAAC TGAAGTCAGC CCAGAAGGAC TTACAGAGTG CTGACAAGGA AATCATGAGC 900  
CTGAAAAAGA AGCTAACGAT GCTGCAGGAA ACCTTGAACC TGCCACCAGT GGCCAGTGAG 960  
ACTGTCGACC GCCTGGTTTT AGAGAGCCCA GCCCCTGTGG AGGTGAATCT GAAGCTCCGC 1020  
CGGCCATCCT TCCGTGATGA TATTGATCTC AATGCTACCT TTGATGTGGA TACTCCCCCA 1080  
GCCCCGCCCT CCAGCTCCCA GCATGGTTAC TACGAAAAAC TTTGCCTAGA GAAGTCACAC 1140  
TCCCCAATTC AGGATGTCCC CAAGAAGATA TGCAAAGGCC CCAGGAAGGA GTCCCAGCTC 1200  
TCACTGGGTG GCCAGAGCTG TGCAGGAGAG CCAGATGAGG AACTGGTTGG TGCCTTCCTT 1260  
ATTTTGTGCC GGAATGCCAT CCTAGGCCAG AAACAGCCCA AAAGGCCAG GTCAGAGTCC 1320  
TCTTGCAGCA AAGATGTGGT AAGGACAGGC TTCGATGGGC TCGGTGGCCG GACAAAATTC 1380  
ATCCAGCCTA CTGACACAGT CATGATCCGC CCATTGCCTG TTAAGCCCAA GACCAAGGTT 1440



AAGCAGAGGG TGAGGGTGAA GACCGTGCCT TCTCTCTTCC AGGCCAAGCT GGACACCTTC 1500  
 CTGTGGTCGT GAGAACAGTG AGTCTGACCA ATGGCCAGAC ACATGCCTGC AACTTGTAGG 1560  
 TCAAGGACTG TCCAGGCAGG GTTTGTGGAC AGAGCCCTAC TTTCGGGACC AGCCTGAGGT 1620  
 GTAAGGGCAG ACAAACAGGT GAGGGTGAGT GTGACACCCA GAGACTGCTC TTCCTGCCCT 1680  
 CACCCTGCCC CACTCCTACG ACTGGGAGCT GACATGACCA GCCCACTGAT CCTGTGAGCA 1740  
 GGTCTTGCTC TGTTGCCAGG CTCTTGTTTA TAGCCATGAT CAGATGTGGT CAGACTCTTT 1800  
 CTGGGCCTGG AGACCACGGT CACTTGTTGA CTGTCTCTGT GGACCAGAGT GCTTGAGGCA 1860  
 TCTCAGGCAG CCTCAGCCCA AGCTTCTACC TGCCTTTGAC TTGCTTCTAG CATAGCCTGG 1920  
 GCCAAGCAGG GTGGGGAATG GAGGATAGAC ATGGGATGTA TGGAGAGGAT GGAAGATTTT 1980  
 CCCGAAAAAA AAAAAAAAAA AAAAAAA 2007

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCACGAGGT GCGGTGGAGC GAAATTTGAA GGAACCGGAG CGGTGGCCGG TTCCACCAAA 60  
 CTGTGTCTGT CTCTGGCAGC TGTTCCCTG GGCTGCTTGA GTCGAGCCAT CATGCCTATC 120  
 CTCTCTCTGT GCACTATCTG CTCCGACTTC TTCGATCACT CCCGTGACGT GGCTGCCATC 180  
 CACTGTGGCC AACTTTTCA TCTGCAATGC CTAATCCAGT GGTTTGAGAC AGCACCAAGT 240  
 CGGACCTGCC CACAGTGTAG AATCCAGGTT GGCAAAAAGA CTATTATAAA CAAACTTTTC 300  
 TTTGACCTCG CCCAGGAAGA GGAGAATGTC TTGGATGCAG AATTCTTAAA GAATGAACTG 360  
 GACAGCGTCA AAGCTCAGCT TTCCCAGAAA GACAGGGAGA AACGGGACAG CCAGGCCATT 420  
 ATCGACACTC TACGGGACAC CCTGGAAGAA CGCAATGCTA CCGTGGAGTC CCTACAGAAC 480  
 GCCTTAAACA AGGCAGAGAT GCTGTGTTCC ACCCTGAAAA AACAGATGAA GTTCCTGGAG 540  
 CAGCGGCAGG ATGAGACCAA ACAAGCTCGG GAGGAGGCC ACCGACTCAA GTGCAAGATG 600  
 AAAACCATGG AGCAAATTGA GTCCTACTC CAGAGCCAGC GTTCTGAGGT GGAGGAGATG 660  
 ATTCGAGACA TGGGTGTGGG ACAGTCAGCG GTGGAGCAGC TGGCTGTGTA CTGCGTGTCC 720  
 CTCAAGAAAG AGTATGAGAA TCTGAAGGAA GCTCGGAAGG CCACAGGGGA ACTGGCTGAC 780

AGGTTGAAGA AGGATTTGGT GTCCTCTAGG AGCAAGTTGA AGACTCTCAA CACTGAGCTG 840  
 GATCAGGCCA AGTTAGAACT GAGGTCAGCC CAGAAGGACT TACAAAGTGC TGACCAGGAG 900  
 ATCACGAGCC TAAGAAAGAA GTCTGATGAT CCTCCAGGGA ACCTTGAGCC TGCCTCCGCG 960  
 ACCAATGAGA CGGTCAGCCG CCTGGTTTTT GAGAGCCCAG CCCCTGTGGA GATGATGAAC 1020  
 CCGAGGCTTC ACCAGCCACC CTTCGGTGAT GAGATTGATC TCAATACCAC CTTTGATGTA 1080  
 AATACCCCTC CAACCCAGAC CTCTGGCTCC CAGCATTGCC TCCCAAGAA GCTGTGCCTG 1140  
 GAGAGGGCAC GCTCTCCCAT GCAGAATGTC CTCAAGAAGG TGCACAAAGT CTCQAAGCCG 1200  
 GAGTCCCAGC TCTCACTGGG TGGCCAGCGA TGTGTAGGAG AGCTAGATGA GGAAGTGGCT 1260  
 GGTGCCTTCC CTCTCTTCAT CCGGAATGCT GTCCTGGGTC AGAAACAGCC CAACAGGACC 1320  
 ACAGCAGAAT CCCGAAGCAG CACAGATGTG GTAAGAATAG GCTTTGATGG GCTTGGAGGA 1380  
 CGAACAAAAT TCATCCAGCC TAGGGACACA ACCATTATCC GACCAATGCC TGTTAAGTCC 1440  
 AAGGCCAAGA GTAAACAGAA AGTGAGAATA AAGACTGTGA GTTCTGCCTC CCAGCCCAAG 1500  
 CTGGATACCT TCTTATGTCA GTGAACGGTG ACCAGAGTGA TGTGTGCAAT TAGTGGGCCA 1560  
 AGACCTGGCT AACCGGAAGT GTTTTTGGAA GATGGCTCCT CTGGACCAG TCCAAGAGAG 1620  
 ATGCCCAGAA AACACACTTC CTGTGTTTAC TGCGCCCTGC ACCACACTGG GAAGCCACAT 1680  
 GACCAGTTTA CTGTTCCGAT CAGCAGGGCC TACTTCCAGT TGCAGGGTTT TGCTTATAGC 1740  
 TACAACCAGG TGTGGCTGGA CTCCTTTTGT TTTTATAGAA CAGGGTCACA TTGACTCTAA 1800  
 GTGGATGGGA GTGCTGGAGG ATCCTATGCA GGCTGGAGGA CCCTGCGCTT GAACTCCTGC 1860  
 CTGCCTCCAG CTTATTGCTT GAAATTATGG GGTGAGGTGG TGATAGGGAA AGGTTGGGGA 1920  
 AGTTTTCTGT GTAAAATAAA AAGGGATCTT TTCTTCAAAA AAAAAAAAAA AAAAA 1975

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 

Lys	Tyr	Leu	Cys	Ser	Ala	Cys	Lys	Asn	Ile	Leu	Arg	Arg	Pro	Phe	Gln
1				5					10					15	
Ala	Gln	Cys	Gly	His	Arg	Tyr	Cys	Ser	Phe	Cys	Leu	Thr	Ser	Ile	Leu
			20					25					30		

Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu Gly Leu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 46 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln  
 1 5 10 15  
 Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu  
 20 25 30  
 Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe  
 1 5 10 15  
 Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu  
 20 25 30  
 Arg Lys Cys Pro Ile Cys Gly Arg Gly Thr Ile  
 35 40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Gln Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys Ile  
1 5 10 15  
Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser Trp Gln  
20 25 30  
Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys Arg Cys Glu Ile Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met Thr  
1 5 10 15  
Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val Thr Ala  
20 25 30  
Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys Lys Leu Val  
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val Ser  
1 5 10 15  
Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln Val Gly  
20 25 30  
Lys Gly Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg Phe Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys  
1 5 10 15  
Leu Arg Ile Leu Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp  
20 25 30  
Pro Trp Leu Thr Lys Thr Lys Lys Thr Cys Pro Val Cys Lys Gln Lys  
35 40 45  
Val Val  
50

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ala Glu Cys Thr Ile Cys Tyr Glu Asn Pro Ile Asp Ser Val Leu  
1 5 10 15

Arg

Crat  
Pl

[illegible]